

SEQUENCE LISTING

<110> Anderson, Christen M.
 Davis, Robert E.
 Clevenger, William
 Wiley, Sandra Eileen
 Willer, Scott W.
 Szabo, Tomas R.
 Ghosh, Soumitra S.
 Moos, Walter H.
 Pei, Yazhong

<120> PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

<130> 660088.420D1

<140> US

<141> 2001-03-14

<160> 37

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 894

<212> DNA

<213> Homo sapien

<400> 1

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gccagcaaac	agatcagtc	tgagaagcag	tacaaaggga	tcattgattg	tgtggtgaga	180
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tacttcccca	cccaagctct	caacttcgcc	ttcaaggaca	agtacaagca	gctcttctta	300
gggggtgtgg	atcggcataa	gcagttctgg	cgctactttg	ctggtaacct	ggcgtccggt	360
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caaggcatca	ttatctatag	agctgcctac	ttcggagtct	atgatactgc	caaggggatg	600
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gcagtcgcag	ggctgctgtc	ctaccccttt	gacactgttc	gtcgtagaat	gatgatgcag	720
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gcaaaagacg	aaggagccaa	ggccttcttc	aaaggtgcct	ggtccaatgt	gctgagagggc	840
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<211> 897

<212> DNA

<213> Homo sapien

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gccagcaagc	agatcactgc	agataagcaa	tacaaaggca	ttatagactg	cgtgggtccgt	180
attcccaagg	agcaggaagt	tctgtccttc	tggcgcggta	acctggccaa	tgtcatcaga	240

tacttcccca	cccaggctct	taacttcgcc	ttcaaagata	aatacaagca	gatcttcctg	300
ggtggtgtgg	acaagagAAC	ccagtttttg	cgctaacttg	cagggaatct	ggcatcgggt	360
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ctagcagctg	atgtgggtaa	agctggagct	gaaagggAat	tccgaggcct	cggtgactgc	480
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gtgcagggtA	ttatcatctA	ccgagccgcc	tacttcggta	tctatgacac	tgcaaaggga	600
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attgctcgtg	atgaaggagg	caaagctttt	ttcaagggtg	catggtccaa	tggtctcaga	840
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gccagcaagc	agatcgccgc	cgacaagcag	tacaagggca	tcgtggactg	cattgtccgc	180
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tacttcccca	ctcaagccct	caacttcgcc	ttcaaggata	agtacaagca	gatcttcctg	300
gggggctggg	acaagcacac	gcagttctgg	aggtactttg	cgggcaacct	ggcctccggc	360
ggtgcggccg	gcgcgacctc	cctctgcttc	gtgtaccctc	tggattttgc	cagaacctgc	420
ctggcagcgg	acgtgggaaa	gtcaggcaca	gagcgcgagt	tccgaggcct	gggagactgc	480
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gtgcagggca	tcacatctta	ccgggcggcc	tacttcggcg	tgtacgatac	ggccaagggc	600
atgctccccg	accccaagaa	cacgcacatc	gtggtgagct	ggatgatcgc	gcagaccgtg	660
acggccgtgg	ccggcgtggt	gtcctacccc	ttcgacacgg	tgccggcgcg	catgatgatg	720
cagtcggggc	gcaaaggagc	tgacatcatg	tacacgggca	ccgtcgactg	ttggaggag	780
atcttcagag	atgagggggg	caaggccttc	ttcaagggtg	cgtggtccaa	cgtcctgcgg	840
ggcatggggg	gcgccctcgt	gctgggtcctg	tacgacgagc	tcaagaaggt	gatctaa	897

<210> 4
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

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<210> 6

<211> 43
 <212> DNA
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<220>
 <223> PCR Primer

<400> 6
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<210> 7
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 7
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<210> 8
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 8
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<210> 9
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 10
 <211> 21
 <212> DNA
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<220>
 <223> Sequence primer

<400> 10
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<210> 11
 <211> 18
 <212> DNA

<213> Artificial Sequence
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 <223> Sequence primer
 <400> 11
 cgccaaaaca gccaagct 18
 <210> 12
 <211> 45
 <212> DNA
 <213> Artificial Sequence
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 <223> Mutagenic oligonucleotide primer
 <400> 12
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 <210> 13
 <211> 45
 <212> DNA
 <213> Artificial Sequence
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 <223> Mutagenic oligonucleotide primer
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 <210> 14
 <211> 35
 <212> DNA
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 <400> 14
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 <212> DNA
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 <223> PCR primer
 <400> 15
 cccgggctcg agttagagtc accttcttga gctc 34
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 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

 <400> 16
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 <210> 17
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 <212> DNA
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 <220>
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 <400> 17
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 <210> 18
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 <212> DNA
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 <220>
 <223> Sequencing primer

 <400> 18
 aaatgataac catctcgc 18

 <210> 19
 <211> 18
 <212> DNA
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 <220>
 <223> Sequencing primer

 <400> 19
 acttcaagga gaatttcc 18

 <210> 20
 <211> 18
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 <220>
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 <400> 20
 acttcgcctt cacggata 18

 <210> 21
 <211> 18
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<400> 21
tacggccaag ggcattct 18

<210> 22
<211> 18
<212> DNA
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<220>
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<400> 22
tgaagcggaa gttcctat 18

<210> 23
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<220>
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<400> 23
atgccggttc ccgtacga 18

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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<400> 24
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<210> 25
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<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer

<400> 25
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<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 26

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41

<210> 27

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 27

ttataggatc cttagatcac cttcttgagc tcgtcgtaca g

41

<210> 28

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 28

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42

<210> 29

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 29

ttatactcga gttagatcac cttcttgagc tcgtcgtaca gg

42

<210> 30

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 30

Cys	Trp	Arg	Lys	Ile	Phe	Arg	Asp	Glu	Gly	Gly	Lys	Ala	Phe	Phe
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<210> 31

<211> 297

<212> PRT

<213> Homo sapien

<400> 31

Met	Gly	Asp	His	Ala	Trp	Ser	Phe	Leu	Lys	Asp	Phe	Leu	Ala	Gly	Ala
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Val	Ala	Ala	Ala	Val	Ser	Lys	Thr	Ala	Val	Ala	Pro	Ile	Glu	Arg	Val
			20					25					30		

Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Ser Ala Glu
 35 40 45
 Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu
 50 55 60
 Gln Gly Phe Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg
 65 70 75 80
 Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
 85 90 95
 Gln Leu Phe Leu Gly Gly Val Asp Arg His Lys Gln Phe Trp Arg Tyr
 100 105 110
 Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
 115 120 125
 Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp
 130 135 140
 Val Gly Arg Arg Ala Gln Arg Glu Phe His Gly Leu Gly Asp Cys Ile
 145 150 155 160
 Ile Lys Ile Phe Lys Ser Asp Gly Leu Arg Gly Leu Tyr Gln Gly Phe
 165 170 175
 Asn Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe Gly
 180 185 190
 Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Val His
 195 200 205
 Ile Phe Val Ser Trp Met Ile Ala Gln Ser Val Thr Ala Val Ala Gly
 210 215 220
 Leu Leu Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met Gln
 225 230 235 240
 Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp Cys
 245 250 255
 Trp Arg Lys Ile Ala Lys Asp Glu Gly Ala Lys Ala Phe Phe Lys Gly
 260 265 270
 Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu Val
 275 280 285
 Leu Tyr Asp Glu Ile Lys Lys Tyr Val
 290 295

<210> 32
 <211> 298
 <212> PRT
 <213> Homo sapien

<400> 32

Met Thr Asp Ala Ala Leu Ser Phe Ala Lys Asp Phe Leu Ala Gly Gly
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 Val Ala Ala Ala Ile Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
 20 25 30
 Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Thr Ala Asp
 35 40 45
 Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu
 50 55 60
 Gln Glu Val Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg
 65 70 75 80
 Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
 85 90 95
 Gln Ile Phe Leu Gly Gly Val Asp Lys Arg Thr Gln Phe Trp Arg Tyr
 100 105 110
 Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
 115 120 125

Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp
 130 135 140
 Val Gly Lys Ala Gly Ala Glu Arg Glu Phe Arg Gly Leu Gly Asp Cys
 145 150 155 160
 Leu Val Lys Ile Tyr Lys Ser Asp Gly Ile Lys Gly Leu Tyr Gln Gly
 165 170 175
 Phe Asn Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe
 180 185 190
 Gly Ile Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr
 195 200 205
 His Ile Val Ile Ser Trp Met Ile Ala Gln Thr Val Thr Ala Val Ala
 210 215 220
 Gly Leu Thr Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met
 225 230 235 240
 Gln Ser Gly Arg Lys Gly Thr Asp Ile Met Tyr Thr Gly Thr Leu Asp
 245 250 255
 Cys Trp Arg Lys Ile Ala Arg Asp Glu Gly Gly Lys Ala Phe Phe Lys
 260 265 270
 Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu
 275 280 285
 Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr
 290 295

<210> 33
 <211> 298
 <212> PRT
 <213> Homo sapien

<400> 33

Met Thr Glu Gln Ala Ile Ser Phe Ala Lys Asp Phe Leu Ala Gly Gly
 1 5 10 15
 Ile Ala Ala Ala Ile Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
 20 25 30
 Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Ala Ala Asp
 35 40 45
 Lys Gln Tyr Lys Gly Ile Val Asp Cys Ile Val Arg Ile Pro Lys Glu
 50 55 60
 Gln Gly Val Leu Ser Phe Thr Arg Gly Asn Leu Ala Asn Val Ile Arg
 65 70 75 80
 Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
 85 90 95
 Gln Ile Phe Leu Gly Gly Val Asp Lys His Thr Gln Phe Trp Arg Tyr
 100 105 110
 Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
 115 120 125
 Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp
 130 135 140
 Val Gly Lys Ser Gly Thr Glu Arg Glu Phe Arg Gly Leu Gly Asp Cys
 145 150 155 160
 Leu Val Lys Ile Thr Lys Ser Asp Gly Ile Arg Gly Leu Tyr Gln Gly
 165 170 175
 Phe Ser Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Tyr Phe
 180 185 190
 Gly Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr
 195 200 205
 His Ile Val Val Ser Trp Met Ile Ala Gln Thr Val Thr Ala Val Ala
 210 215 220

Gly Val Val Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met
 225 230 235 240
 Gln Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp
 245 250 255
 Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Gly Lys Ala Phe Phe Lys
 260 265 270
 Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu
 275 280 285
 Val Leu Tyr Asp Glu Leu Lys Lys Val Ile
 290 295

<210> 34
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for PCR amplification of human ANT3 for
 expression construct

<400> 34
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<210> 35
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for PCR amplification of human ANT3 for
 expression construct

<400> 35
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<210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for PCR amplification of EYFP

<400> 36
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<210> 37
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for PCR amplification of EYFP

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